

## **DNA sequences in Enchytraeidae taxonomy, a progress report**

***SCHMELZ Rüdiger M.<sup>1,2</sup>, COLLADO Rut<sup>1</sup>, PORCO David<sup>3</sup>, VIERA Joaquín<sup>4</sup>, RÖMBKE Jörg<sup>1</sup>***

<sup>1</sup>*ECT Oekotoxikologie GmbH, Flörsheim, Germany*

<sup>2</sup>*University of A Coruña, Science Faculty, Department of Animal Biology, Plant Biology and Ecology, Spain*

<sup>3</sup>*Université de Rouen, Laboratoire ECODIV, Mont Saint Aignan, France*

<sup>4</sup>*AllGenetics, A Coruña, Campus de Elviña, Spain*

*e-mail: rmschmelz@gmail.com, j-roembke@ect.de, rutco@udc.de, david.porco.gm@gmail.com, joaquin@allgenetics.eu*

Taxonomy of enchytraeids is usually lagging behind the current trends, but the last five years have seen an increasing integration of DNA sequences into the taxonomic and systematic work with this group. Reviewing the literature and reporting work in progress of our own initiatives, we give an account of the state of the art and we critically assess the potential of DNA sequences in Enchytraeidae taxonomy using a few case studies as examples. DNA sequences provide an independent second dataset that allows to falsify or to confirm hypotheses based on morphological work. Molecular phylogenies help to interpret character changes and evolution within the group, which means nothing less than to understand the extant patterns of diversity. At the species level DNA sequences have unveiled cryptic diversity but also the contrary, synonymies of species. Large-scale barcoding of common terrestrial species may allow automated sequence-based identification of selected sites in the near future. Together with sound morphological work, DNA-based taxonomy opens a new era of Natural History.

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